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RAW SEQUENCE LISTING

DATE: 07/25/2001

PATENT APPLICATION: US/09/771,382

TIME: 12:36:39

Input Set : A:\8795_24U1.txt

Output Set: N:\CRF3\07252001\I771382.raw

PS

ENTERED

3 <110> APPLICANT: Peak, Ian
 4 Jennings, Michael
 6 <120> TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
 8 <130> FILE REFERENCE: 8795-24U1
 10 <140> CURRENT APPLICATION NUMBER: US 09/771,382
 11 <141> CURRENT FILING DATE: 2001-01-25
 13 <150> PRIOR APPLICATION NUMBER: US 60/177,917
 14 <151> PRIOR FILING DATE: 2000-01-25
 16 <160> NUMBER OF SEQ ID NOS: 52
 18 <170> SOFTWARE: PatentIn version 3.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 591
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Neisseria meningitidis
 25 <400> SEQUENCE: 1
 27 Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
 28 1 5 10 15
 30 Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
 31 20 25 30
 33 Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
 34 35 40 45
 36 Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro
 37 50 55 60
 39 Val Gln Arg Thr Val Ala Val Leu Ile Val Asn Ser Asp Lys Glu Gly
 40 65 70 75 80
 42 Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr
 43 85 90 95
 45 Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala
 46 100 105 110
 48 Gly Asp Asn Leu Lys Ile Lys Gln Asn Gly Thr Asn Phe Thr Tyr Ser
 49 115 120 125
 51 Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu Lys Leu
 52 130 135 140
 54 Ser Phe Ser Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys
 55 145 150 155 160
 57 Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
 58 165 170 175
 60 Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Leu Asn
 61 180 185 190
 63 Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu
 64 195 200 205
 66 Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn
 67 210 215 220
 69 Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe
 70 225 230 235 240
 72 Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
 73 245 250 255

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75 Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val
76          260          265          270
78 Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
79          275          280          285
81 Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
82          290          295          300
84 Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala
85 305          310          315          320
87 Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
88          325          330          335
90 Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
91          340          345          350
93 Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
94          355          360          365
96 Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
97          370          375          380
99 Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser
100 385          390          395          400
102 Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
103          405          410          415
105 Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
106          420          425          430
108 Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
109          435          440          445
111 Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
112          450          455          460
114 Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg
115 465          470          475          480
117 Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val
118          485          490          495
120 Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn
121          500          505          510
123 Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala
124          515          520          525
126 Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly
127          530          535          540
129 Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser
130 545          550          555          560
132 Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly Asn
133          565          570          575
135 Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
136          580          585          590
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 592
140 <212> TYPE: PRT
141 <213> ORGANISM: Neisseria meningitidis
143 <400> SEQUENCE: 2
145 Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
146 1          5          10          15

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```

148 Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
149          20          25          30
151 Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
152          35          40          45
154 Ala Asn Ala Thr Asp Glu Asp Glu Glu Glu Leu Glu Ser Val Gln
155          50          55          60
157 Arg Ser Val Val Gly Ser Ile Gln Ala Ser Met Glu Gly Ser Val Glu
158 65          70          75          80
160 Leu Glu Thr Ile Ser Leu Ser Met Thr Asn Asp Ser Lys Glu Phe Val
161          85          90          95
163 Asp Pro Tyr Ile Val Val Thr Leu Lys Ala Gly Asp Asn Leu Lys Ile
164          100         105         110
166 Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala Ser Ser Phe Thr Tyr Ser
167          115         120         125
169 Leu Lys Lys Asp Leu Thr Gly Leu Ile Asn Val Glu Thr Glu Lys Leu
170          130         135         140
172 Ser Phe Gly Ala Asn Gly Lys Lys Val Asn Ile Ile Ser Asp Thr Lys
173 145          150         155         160
175 Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
176          165         170         175
178 Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Met Leu Leu Asn
179          180         185         190
181 Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu
182          195         200         205
184 Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn
185          210         215         220
187 Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe
188 225          230         235         240
190 Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
191          245         250         255
193 Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val
194          260         265         270
196 Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
197          275         280         285
199 Val Thr Gly Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
200          290         295         300
202 Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala
203 305          310         315         320
205 Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
206          325         330         335
208 Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Lys Val Thr Phe Ala Ser
209          340         345         350
211 Gly Asn Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
212          355         360         365
214 Thr Val Lys Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
215          370         375         380
217 Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser
218 385          390         395         400
220 Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met

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```

221          405          410          415
223 Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
224          420          425          430
226 Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
227          435          440          445
229 Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
230          450          455          460
232 Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val
233 465          470          475          480
235 Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn
236          485          490          495
238 Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp
239          500          505          510
241 Asn Val Asn Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr
242          515          520          525
244 Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile
245          530          535          540
247 Gly Gly Gly Thr Tyr Leu Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser
248 545          550          555          560
250 Ser Ile Ser Ala Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly
251          565          570          575
253 Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
254          580          585          590
256 <210> SEQ ID NO: 3
257 <211> LENGTH: 589
258 <212> TYPE: PRT
259 <213> ORGANISM: Neisseria meningitidis
261 <400> SEQUENCE: 3
263 Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
264 1          5          10          15
266 Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
267          20          25          30
269 Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Ser Ala Thr Val Gln
270          35          40          45
272 Ala Asn Ala Thr Asp Thr Asp Glu Asp Glu Glu Leu Glu Ser Val Ala
273          50          55          60
275 Arg Ser Ala Leu Val Leu Gln Phe Met Ile Asp Lys Glu Gly Asn Gly
276 65          70          75          80
278 Glu Ile Glu Ser Thr Gly Asp Ile Gly Trp Ser Ile Tyr Tyr Asp Asp
279          85          90          95
281 His Asn Thr Leu His Gly Ala Thr Val Thr Leu Lys Ala Gly Asp Asn
282          100          105          110
284 Leu Lys Ile Lys Gln Ser Gly Lys Asp Phe Thr Tyr Ser Leu Lys Lys
285          115          120          125
287 Glu Leu Lys Asp Leu Thr Ser Val Glu Thr Glu Lys Leu Ser Phe Gly
288          130          135          140
290 Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys Gly Leu Asn
291 145          150          155          160
293 Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Pro Thr Val His Leu

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```

294          165          170          175
296 Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Ala Gly Ser Ser Ala
297          180          185          190
299 Ser His Val Asp Ala Gly Asn Gln Ser Thr His Tyr Thr Arg Ala Ala
300          195          200          205
302 Ser Ile Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys Gly Val Lys
303          210          215          220
305 Thr Gly Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe Val Arg Thr
306 225          230          235          240
308 Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr Thr Thr Val
309          245          250          255
311 Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr Glu Val Lys Ile Gly
312          260          265          270
314 Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu Val Thr Gly
315          275          280          285
317 Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly Glu Gly Leu
318          290          295          300
320 Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala Gly Trp Arg
321 305          310          315          320
323 Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala Asp Lys Phe
324          325          330          335
326 Glu Thr Val Thr Ser Gly Thr Lys Val Thr Phe Ala Ser Gly Asn Gly
327          340          345          350
329 Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile Thr Val Lys
330          355          360          365
332 Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln Leu Gln Asn
333          370          375          380
335 Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser Ser Gly Lys
336 385          390          395          400
338 Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met Asp Glu Thr
339          405          410          415
341 Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg Asn Gly Lys
342          420          425          430
344 Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser Ser Val Ser
345          435          440          445
347 Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp Asp Glu Gly
348          450          455          460
350 Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val Arg Ile Thr
351 465          470          475          480
353 Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val Ala Gln
354          485          490          495
356 Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn Val Asn
357          500          505          510
359 Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala Gly Leu
360          515          520          525
362 Ala Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly Gly Gly
363          530          535          540
365 Thr Tyr Leu Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser Ile Ser
366 545          550          555          560

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\8795_24U1.txt

Output Set: N:\CRF3\07252001\I771382.raw

L:1228 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1231 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1234 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1237 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1240 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1243 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1246 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1249 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1252 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1255 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1258 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1261 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1261 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1264 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1267 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1273 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1279 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1285 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1294 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1297 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1309 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1312 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1315 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1318 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11

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Input Set : A:\8795_24U1.txt

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L:1324 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1327 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1330 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1333 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1336 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1339 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:1339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:2024 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2024 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2026 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2026 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2028 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2030 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2030 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2032 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2032 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2034 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2036 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2036 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2038 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2038 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2040 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2040 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2042 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2044 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2046 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2046 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2048 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2048 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2052 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2052 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2054 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2054 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2058 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2060 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2060 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2062 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:2062 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2068 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22

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L:2068 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22

L:2070 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22

L:2070 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22